

RL Int. J. Pept. Protein Res. 22:476-481(1983).
 CC -!- FUNCTION: NOT KNOWN.
 CC -!- SIMILARITY: STRONG, TO TURKEY MELEAGRIN, AND SOME, TO A PART
 CC (EXON 9) OF TRANSFERRINS.
 DR PIR: R03258; IZWS.
 KW Egg white.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 6 33 OR 6-32 (BY SIMILARITY).
 FT DISULFID 12 28 BY SIMILARITY.
 FT DISULFID 16 32 OR 16-33 (BY SIMILARITY).
 SQ SEQUENCE 39 AA: 4452 MW: 8D5DE270495FB4A4 CRC64;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RN OC Ephydriidae; drosophilidae; Drosophila.
 RP SEQUENCE FROM N.A.
 RC STRAIN-OREGON R;
 RX MEDLINE=92102953; PubMed=1684716;
 RA Kuhn R., Kuhn C., Beersch D., Glaetzer K.H., Schaefer U.,
 RA Schaefer M.;
 RA "A cluster of four genes selectively expressed in the male germ line
 RT of *Drosophila melanogaster*";
 RL Mech. Dev. 35:143-151(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blakej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Frankoch C., Baldwin D.,
 RA Ballova R.M., Basu A., Boxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burcik K.C., Busam D.A., Butler H., Cadieu E., Centner A., Chandria I.,
 RA Cherry J.M., Cawley S., Dahlke C., Andrews-Frankoch C., Baldwin D.,
 RA de Pablo J.B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy L., Muzyk D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klaimos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirkas R., Tector C., Turner R., Verete E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 CC -!- TISSUE SPECIFICITY: TESTIS.
 CC -!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCTYES.
 CC -!- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
 MOTIFS.
 CC -!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; AE003672; AAF54025.1; -
 DR EMBL; AE003672; AAF54025.1; -
 DR HSSP; P01180; INPO.
 DR FLXBASE; FBn0004174; Mst84DC.
 KW Sporadogenesis; Repeat; Multigene family.
 SQ SEQUENCE 55 AA: 5225 MW: 95A12F3ABC88BD6C CRC64;
 OC Drosophila melanogaster (Fruit fly);
 OC Metazoa; Arthropoda; Insecta; Diptera; Brachycera; Muscomorpha;
 OC Eukaryota; Neoptera; Endopterygota;
 OC Pterygota;
 OS Drosophila melanogaster (Fruit fly);
 OS Drosophila; Metazoa; Arthropoda; Insecta; Diptera; Brachycera; Muscomorpha;

		Query Match	Score 53; DB 1; Length 55;
		Best Local Similarity	19.0%; Pred. No. 52;
		Matches	4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;
QY	1	CXXXCXXXXXXCXXXC 21	
	2	CCGCGSCCGYCCGPGC 22	
RESULT	5		
ID	AMCI_APIME	STANDARD;	PRT;
AC	P5662;		56 AA.
DT	15-JUL-1999 (Rel. 38, Created)		
DT	15-JUL-1999 (Rel. 38, Last sequence update)		
DT	30-MAY-2000 (Rel. 39, Last annotation update)		
DE	CHYMOTRYPsin INHIBITOR (AMCI).		
OS	Apis mellifera (Honeybee).		
OC	Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;		
OC	Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;		
OC	Apoidea; Apidae; Apis.		
[1]	SEQUENCE, AND STRUCTURE BY NMR.		
RC	TISSUE:HEMOLYMPH;		
RX	MEDLINE=9339935; PubMed=10411628;		
RA	Bania J., Stachowiak D., Polanowski A.;		
RT	"Primary structure and properties of the cathepsin G/chymotrypsin inhibitor from the larval hemolymph of <i>Apis mellifera</i> ."		
RT	Eur. J. Biochem. 262:680-687(1999).		
-!-	FUNCTION: CHYMOTRYPsin AND CATHERSPIN G INHIBITOR.		
-!-	SUBCELLULAR LOCATION: SECRETED.		
PDB:	IICCV; 12-MAR-99.		
DR	INTERPRO: IPR002919; -.		
KW	PRAM; PF01826; TIL; 1.		
DR	Proteinase inhibitor; 3D-structure.		
FT	DISULFID 3 36		
FT	DISULFID 12 32		
FT	DISULFID 16 28		
FT	DISULFID 20 56		
FT	DISULFID 38 50		
SO	SEQUENCE 56 AA: 5973 MW:	092B2815AE6B2B7F CRC64;	
RESULT	6		
Query Match	100.0%; Score 53; DB 1; Length 56;		
Best Local Similarity	19.0%; Pred. No. 53;		
Matches	4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;		
QY	1 CXXXCXXXXXXCXXXC 21		
	12 CGSACAPTAQPKTRCTMQC 32		
Db			
RESULT	7		
ID	MTL_HOMAM	STANDARD;	PRT;
AC	P29499;		58 AA.
DT	01-APR-1993 (Rel. 25, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last annotation update)		
DE	METALLOTHIONEIN-1 (COMT-1).		
OS	Homarus americanus (American Lobster).		
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucardiida; Decapoda; Pleocyemata; Astacidae; Nephropoidea; Nephropidae; Homarus.		
OC	Scylla serrata (Mud crab).		
OS	Scylla serrata (Mud crab).		
OC	Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca; Eumalacostraca; Bucardiida; Decapoda; Pleocyemata; Brachyura; Brachyura; Portunoidea; Portunidae; Scylla.		
[1]	SEQUENCE.		
RX	MEDLINE=2142340; PubMed=7061431;		
RA	Leich K., Ammer D., Olafson R.W.;		
RT	"Crab metallothionein. Primary structures of metallothioneins 1 and 2.";		
RL	J. Biol. Chem. 257:2420-2425(1982).		
CC	-!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE RESIDUES THAT BIND VARIOUS HEAVY METALS. THE DIFFERENT BIOLOGICAL FORMS OF LOBSTER METALLOTHIONEINS MAY HAVE DIFFERENT BIOLOGICAL FUNCTIONS.		

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXCXXXXXXXXXXXXXXCXXC 21
 |::|::|::|::|::|::|::|::|:
 Db 34 CSSGCKCTTKEDCKKCTKPC 54

RESULT 12
 MT_POTPO ID MT_POTPO STANDARD; PRT; 58 AA.
 AC P55952;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN (MT).
 OS Potamon potamios.
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidea; Geryonidae; Potamona.
 RN [1]
 RP TISSUE=Midgut;
 RX MEDLINE=9079219; PubMed=8921011;
 RA Pedersen S N., Pedersen K L., Hoejrup P., Depledge M H., Knudsen J.;
 RT "primary structures of decapod crustacean metallothioneins with
 special emphasis on freshwater and semi-terrestrial species";
 RL Biochem. J. 319:99-1003(1996).
 CC -!- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 RESIDUES THAT BIND VARIOUS HEAVY METALS. CLASS I MTS IN CRUSTACEA
 ARE INVOLVED IN THE SEQUESTRATION OF Elevated LEVELS OF HEAVY-
 METAL IONS.
 CC -!- INDUCTION: BY CADMIUM.
 CC -!- MASS SPECTROMETRY: MM=6156.8; METHOD=MALDI.
 CC -!- SIMILARITY: BELONGS TO FAMILY 3 IN METALLOTHIONEIN SUPERFAMILY.
 DR HSSP_P55949, 1DMD.
 DR INTERPRO; IPR002045; -.
 DR INTERPRO; IPR003019; -.
 DR PRINTS; PRO00131; metathio: 1.
 DR PRINTS; PR00858; MICRUSTACEAN.
 KW Metal-binding; Metal-thiolate cluster; Chelation; Cadmium.
 FT DOMAIN 1 29 BETA.
 FT DOMAIN 30 58 ALPHA.
 FT METAL 4 4 CLUSTER B.
 FT METAL 5 5 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 45 45 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 SQ SEQUENCE 58 AA.; 6157 MW; DCB71F9AB4DD779C CRC64;

Query Match 100.0%; Score 53; DB 1; Length 58;
 Best Local Similarity 19.0%; Pred. No. 54; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXXXXXCXXC 21
 |::|::|::|::|::|::|::|::|:
 Db 34 CTSGCKCATKECKTCCKPC 54

RESULT 13
 MT1_CALSI STANDARD; PRT; 59 AA.
 AC P55949;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN-I (MT-I) (MT-IB/MT-TA).
 OS Callinectes sapidus (Blue crab).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
 OC Brachyura; Portunoidea; Geryonidae; Potamona.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=96033062; PubMed=7487904;
 RA Brouwer M., Engbeld J., Hoexum-Brouwer T., Thogersen I., Truncali A.;
 RT "Primary structure and tissue-specific expression of blue crab
 (Callinectes sapidus) metallothionein isoforms.";
 RL Biochem. J. 311:617-622(1995).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=95119049; PubMed=7819257;
 RA Narula S.S., Brouwer M., Hua Y., Armitage I.M.;
 RT "Three-dimensional solution structure of Callinectes sapidus
 metallothionein-1 determined by homonuclear and heteronuclear
 magnetic resonance spectroscopy.";
 RL Biochemistry 34:620-631(1995).
 CC -!- FUNCTION: BINDS SIX DIVALENT METAL IONS. KNOWN TO BIND COPPER AND
 CADMIUM.
 DR INTERPRO; IPR002045; -.
 DR INTERPRO; IPR003019; -.
 DR PRINTS; PF00131; metathio: 1.
 DR PRINTS; PR00858; MICRUSTACEAN.
 KW Metal-binding; Metal-thiolate cluster; Chelation; Copper; Cadmium;
 KW 3D-structure.
 FT DOMAIN 1 29 BETA.
 FT DOMAIN 30 59 ALPHA.
 FT METAL 5 5 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 10 10 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 21 21 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 38 38 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 45 45 CLUSTER A.
 FT METAL 50 50 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 57 57 CLUSTER A.
 FT VARIANT 1 1 MISSING (IN MT-1A);
 SQ SEQUENCE 59 AA.; 6141 MW; 439BB0A9DIA96D34 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 59;
 Best Local Similarity 19.0%; Pred. No. 55; Mismatches 0; Indels 0; Gaps 0;
 Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXXXXXCXXC 21
 |::|::|::|::|::|::|::|::|:
 Db 34 CTSGCKCATKECKTCCKPC 54

RESULT 14
 MT1_CANGA STANDARD; PRT: 62 AA.
 ID MT1_CANGA STANDARD; PRT: 62 AA.
 AC P1513;
 DT 01-APR-1990 (Rel. 14, created)
 DT 01-NOV-1997 (Rel. 35, last annotation update)
 DE METALLOTHIONEIN-1.
 GN MT-I.
 OS Candida glabrata (Yeast); *Torulopsis glabrata*; *Candida*.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; *Candida*.
 OC anamorphic Saccharomycetales; *Candida*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90062075; PubMed=2584191;
 RA Meira R.K., Garey J.R., Butt T.R., Gray W.R., Winge D.R.;
 RT "Candida glabrata metallothioneins. Cloning and sequence of the genes
 and characterization of proteins";
 RL J. Biol. Chem. 264:19747-19753(1989).
 RN [2]
 RP SEQUENCE OF 1-16.
 RX MEDLINE=89105829; PubMed=3194392;
 RA Mehra R.K., Tarbet B.E., Gray W.R., Winge D.R.;
 RT "Metal-specific synthesis of two metallothioneins and gamma-glutamyl
 peptides in *Candida glabrata*";
 PROC. NATL. ACADEM. SCI. U.S.A. 85:8815-8819(1988).
 -!- FUNCTION: THE METALLOTHIONEINS ARE INVOLVED IN THE CELLULAR
 SEQUESTRATION OF TOXIC METAL IONS
 -!- INDUCTION: BOTH MT-I AND MT-II GENES ARE REGULATED BY COPPER ION
 IN A CONCENTRATION-DEPENDENT FASHION, AND BOTH ARE INDUCIBLE BY
 SILVER BUT NOT BY CADMUM SALTS.
 -!- MISCELLANEOUS: MT-I MIGHT BIND APPROXIMATELY 11-12 MOLE OF
 CUT1).

-!- SIMILARITY: BELONGS TO FAMILY 9 IN METALLOTHIONEIN SUPERFAMILY.

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CC CC
 CC EMBL; J05133; AAA35272.1; -. DR DR
 CC PIR; A31252; A31252. DR DR
 CC HSSP; P04355; 4M2Z. DR DR
 KW INIT_MOT_0 REPEAT 22 29 FT FT
 REPEAT 55 62 SQ SEQUENCE 62 AA; 6243 MW: 800768C06C44F7A1 CRC64;

Query Match 100.0%; Score 53; DB 1; Length 62;
 Best local similarity 19.0%; PPrd. No. 55; Matches 4; Conservative 17; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXXXXXXXXXXXXXXC 21 Db 6 CPNGCSCPNCANGGCCGDKC 26

RESULT 15
 M84A_DROME STANDARD; PRT: 63 AA.
 ID M84A_DROME STANDARD; PRT: 63 AA.
 AC 001642; Q9VTA3;
 DT 01-JUL-1993 (Rel. 26, created)
 DT 01-JUL-1993 (Rel. 26, last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE MALE SPECIFIC SPERM PROTEIN MST84DA.
 GN MST84DA.

OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; *Drosophila*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinski S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananades P.G., Scheer S.E., Li P.W., Hoskins R.A., Gille R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Chapple M., Preifer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G.,
 RA Abrol J.F., Agbaria A., An H.-J., Andrews-Pfannkoch C., Baldwin P.,
 RA Ballou R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bernier B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Botchkina M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Danihe C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Douc L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabrilian A.E., Garg N.S., Gelbart W.M., Glisser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Hoek J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matteei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Moharry C., Morris J., Moshefi A.,
 RA Mount S.M., Moy M., Murphy B., Murzy L., Muzzey D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nussbaum D.R., Paciorek J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirkas R., Teeter C., Turner R., Wenter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA RT "The genome sequence of *Drosophila melanogaster*";
 RL Science 287:2185-2195(2000).
 CC -!- TISSUE SPECIFICITY: TESTIS.
 CC -!- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
 CC -!- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPETITIVE C-G-P
 CC MOTIFS.
 CC -!- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.

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CC CC
 CC EMBL; X67703; CAA47937.1; -. DR DR
 DR EMBL; AE005672; AAF54022.1; -. DR DR
 DR HSSP; P01180; INPO. DR DR
 DR FLYBASE; FBgn0004172; Mst84Da.

KW Spermatogenesis; Repeat; Multigene family.
SQ SEQUENCE 63 AA; 5806 MW; BF84CD74CBCEFD3F CRC64;

Search completed: March 1, 2001, 16:26:04
Job time: 401 sec